REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 16, 17 23, 24 and 25 have been amended, and claim 26 has been added. No new matter is being presented, and approval and entry are respectfully requested.

Claims 16, 17, and 23-26 are pending and under consideration. Reconsideration is respectfully requested.

REJECTION UNDER 35 U.S.C. §102:

In the Office Action, at pages 3-5, claims 16, 17 and 23-25 were rejected under 35 U.S.C. §102(b) as being anticipated by Pantoliano et al. (USPN 4,853,871; hereafter, Pantoliano) or Holak et al. (J. Mol. Biol., 210, 635-648; hereafter, Holak) or Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045; hereafter Flaherty) or Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992; hereafter, Mosimann). This rejection is traversed and reconsideration is requested.

Since an application is anticipated only if a single prior art reference discloses each and every limitation of the claimed invention, each of the four cited references will be considered separately.

Independent claims 16, 23, and 24 have been amended for clarity, the terminology "automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence" has been moved from the preamble to the body of the claim, and to show more clearly that calculating a root mean square distance between all of the elements corresponding in the optimum correspondence includes automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence.

Hence, independent claims 16, 23 and 24 are now submitted to distinguish over Pantoliano et al. or Holak or Flaherty or Mosimann, as is set forth with greater particularity below.

Pantoliano recites a method and a system of evaluating a protein's structure to determine whether the protein contains at last two target amino acid residues, replacement of at least one of which with a cystein residue would be sufficient to permit formation of at least one potentially protein-stabilizing disulfide bond. Hence, Pantoliano recites an examination of

amino acid residues to determine if they contain atoms whose relative three-dimensional positions possess a geometric conformation similar to corresponding atoms of a known disulfide bridge, and does not, for example, recite automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is recited in amended independent claims 16, 23 and 24.

Hence, Pantoliano does not recite a method of determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence, comprising:dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and calculating a root mean square distance between all of the elements corresponding in the optimum correspondence to automatically determine a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is recited in amended claim 16, and similarly in amended claims 23 and 24.

Hence, it is respectfully submitted that amended independent claims 16, 23 and 24 are not anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871). Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871) for at least the reasons that amended independent claims 16 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871).

It is respectfully submitted that Holak recites a determination of a three-dimensional structure of a trypsin inhibitor from squash seeds by using 324 interproton distance constraints, 80 non-nuclear Overhauser effect distances, and 22 hydrogen-bonding constraints,

supplemented by 27 φ backbone angle constraints derived from nuclear magnetic resonance measurements, wherein the nuclear magnetic resonance input data were converted to the distance constraints in a semiquantitative manner after a sequence specific assignment of ^1H spectra was obtained using two-dimensional nuclear magnetic resonance techniques and stereospecific assignments were obtained for 17 of the 48 prochiral centers of the squash trypsin inhibitor using the floating chirality assignment introduced at the dynamical simulated annealing stage of the calculations. That is, Holak recites a hybrid method of determining the three-dimensional structure of CMTI-I (from the squash seeds), wherein the hybrid method includes using nuclear magnetic resonance input data, and a "floating" chirality assignment in the simulated annealing stage of the structures calculations to obtain stereospecific assignments at prochiral centers. The present invention does not convert nuclear magnetic resonance input data and does not utilize "floating" chirality assignment.

Holak does not recite automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is recited in amended independent claims 16, 23 and 24.

Hence, Holak does not recite recite a method of determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence, comprising:dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and calculating a root mean square distance between all of the elements corresponding in the optimum correspondence to automatically determine a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is

recited in amended claim 16, and similarly in amended claims 23 and 24.

Hence, it is respectfully submitted that amended independent claims 16, 23 and 24 are not anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol. Biol., 210, 635-648). Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol. Biol., 210, 635-648) for at least the reasons that amended independent claims 16 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol. Biol., 210, 635-648).

Flaherty recites: "The superimposed molecules were inspected by eye to guide the classifications of C_α positions into equivalent, such as corresponding atoms in aligned α-helices and β strands, versus not equivalent, such as those in loops that traverse different routes or are of different lengths." (see col. 2, last full paragraph, p. 5041). Hence, it is respectfully submitted that Flaherty recites an empirical identification of equivalent residues in preference to computational methods that rely primarily on distance criteria (see col. 2, last full paragraph, p. 5041), and teaches away from the present claimed invention, which recites using a computational method.

In addition, Flaherty does not, for example, recite automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is recited in amended independent claims 16, 23 and 24.

Hence, Flaherty does not recite recite a method of determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence, comprising:dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and calculating a root mean square distance between all of the elements corresponding in the optimum correspondence to automatically determine a distance between the elements of the first point

set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest ~~degree of similarity~~correspondence to the input amino acid sequence, as is recited in amended claim 16, and similarly in amended claims 23 and 24.

Hence, it is respectfully submitted that amended independent claims 16, 23 and 24 are not anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045). Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045) for at least the reasons that amended independent claims 16 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045).

Mosimann recites preparing a molecular model of P-30 protein based upon a three-dimensional structure of bovine pancreatic RNase A by inspecting the RNase A structure before amino acids of the P-30 protein were assigned the coordinates of the RNase A template, adjusting side chain torsion angles, minimizing energy of the model to optimize stereochemical geometry and relieving any remaining unacceptably close contacts to retain the essential features of RNase A. The present invention does not recite adjusting side chain torsion angles or minimizing energy of a model to optimize stereochemical geometry and removing unacceptably close contacts.

Hence, Mosimann does not recite recite a method of determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence, comprising:dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and calculating a root mean square distance between all of the elements corresponding in the optimum correspondence to automatically determine a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character

sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence, as is recited in amended claim 16, and similarly in amended claims 23 and 24.

Hence, it is respectfully submitted that amended independent claims 16, 23 and 24 are not anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992). Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992) for at least the reasons that amended independent claims 16 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992).

NEW CLAIM:

New claim 26 recites that the features of the present invention include a computer-readable medium containing computer-readable instructions to compare spatially similar portions of an input amino acid sequence and an amino acid sequence taken from an amino acid sequence database or a motif database, the computer-readable instructions comprising: searching the amino acid sequence database and the motif database for an amino acid sequence or sequences having at least a predetermined degree of similarity to the input amino acid sequence; determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest degree of similarity to the input amino acid sequence, wherein the amino acid sequence having the greatest degree of similarity is selected from a set of amino acid sequences having at least the predetermined degree of similarity; determining the LCS and an occurrence position of the LCS between the character sequence expressing the input amino acid sequence and the character sequence having the greatest degree of similarity and expressing an amino acid sequence taken from the amino acid sequence database or the motif database; and aligning the character sequence of the input amino acid sequence with the character sequence having the greatest degree of similarity and expressing the amino acid sequence from the amino acid sequence database or the motif database, based on the LCS and the occurrence position of the LCS, by inserting a blank corresponding to a length of a character sequence between positions of subsequences.

The new claim is supported by FIG. 1 and pages 16-17 of the specification. Nothing in the prior art teaches or suggests such. It is submitted that this new claim, which is different from prior filed claims, distinguishes over the prior art.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited. At a minimum, this Amendment should be entered at least for purposes of Appeal as it either clarifies and/or narrows the issues for consideration by the Board.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited and possibly concluded by the Examiner contacting the undersigned attorney for a telephone interview to discuss any such remaining issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

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